umbe Chan	ged a file from non-ASCII to ASCII ENTERED Edited by:(STIC
Chan	ged the margins in cases where the sequence text was "wrapped" down to the next line.
Edited	d a format error in the Current Application Data section, specifically:
Edited applic	the Current Application Data section with the actual current number. The number inputted by the ant was the prior application data; or other
Added	the mandatory heading and subheadings for "Current Application Data".
Edited	the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
Chang	ged the spelling of a mandatory field (the headings or subheadings), specifically:
Corre	cted the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
nserte	ed or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
Correc	ted subheading placement. All responses must be on the same line as each subheading. If the ant placed a response below the subheading, this was moved to its appropriate place.
Insert	ed colons after headings/subheadings. Headings edited included:
Delet	ed extra, invalid, headings used by an applicant, specifically:
Delet	ed: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of flage numbers throughout text; other invalid text, such as
Inser	led mandatory headings, specifically:
Corre	cted an obvious error in the response, specifically:
Edite	d identifiers where upper case is used but lower case is required, or vice versa.
	cted an error in the Number of Sequences field, specifically:
A *Ha	rd Page Break* code was inserted by the applicant. All occurrences had to be deleted.
elete ue to	d endIng stop codon in ampo acid sequences and adjusted the "(A)Length:" field accordingly (erro a PatentIn bug). Sequences corrected:
Other	:

Examiner: The above corrections must be communicated to the applicant in the first Office 3/1/95 Action. DO NOT send a copy of this form.



OIPE

RAW SEQUENCE LISTING

HATENT APPLICATION: US/10/087,190

PATE: 01/19/2003 TIME: 19:EV:25

Input Set : N:\AMC\087190.txt

Output Set: N:\CRF4\02192003\J087190.raw

```
4 <110 - AFFLICANT: Agensys, Inc.
             Challita-Eid, Pia M.
              Hubert, Kene S.
             Raitano, Arthur B.
             Far.s, Mary
             Afar, Daniel E. H.
             Ge, Wangmao
     1(
             Jakobovit:, Aya
     15 <1200 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
            ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
     1.;
     1" <130> FILE PEFERENCE: 51158-20034.20
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/087,190
C--> 20 <141> CURRENT FILING DATE: 2003-01-28
     II <150> PRIOR APPLICATION NUMBER: US 09/779,250
     : - <151> FRIOR FILING DATE: 2001-03-05
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     11 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     -0 <211> LENGTH: 254
     -1 <212> TYPE: DNA
     -2 <213> ORGANISM: Homo Sapiens
     54 <400> SEQUENCE: 1
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     ni hagaaagete tittgetage etggtteget etteegttte acateggeea attttagett 120
     b) totoaatgot titotgtagg oftgoatgot titgactico ofcagacaac tgagaticca 180
     эн gaacctccsa citatgitto citgoatgaa gagctttact iggaaaagcc caataataat 240
     3+ tagaagttös dato
     41 <210> SEQ ID NO: 2
     43 <211> LENGTH: 867
     43 <212> TYPE: DNA
     44 <213> ORGANISM: Homo Sapiens
     46 WARGH FEMTURE:
     47 <221> NAME/REY: CDS
     43 <2220 LOCATION: (82)...(696)
     50 K400% SEQUENCE: 1
     51 ocaavaticaa angogtioogg gootigtioogg coodtotood caagegoggg cooggonage 60
     52 ggaagereet gracerjege e aku kea aag aaa aaa gga ekg agt gea gaa
                                Most Ser Lys Lys Lys Gly Lou Ser Ala Glu
     53
     54
     56 qua adinaga art inclatif atin qaa ata tit tot daa ata aaa gat ita
     87 Glu Lys Arg Thr Ara Met Mot Win lie The Ber 3lu Thr Lys Asp Val
                                             2.()
                         15
     60 tit cas tts and pay tig god and att let oec aso day and ggs att
```

RAW SEQUENCE LISTING PATE: % 100. STATE: % 1

Input Set : N:\AMC\087190.txt

Output Set: N:\CRF4\02192003\J087190.raw

čl Phe Gln Leu 62	Lys Asp Leu Glu I	Lys lle Ala Pro Lys (Glu Lys Gly 11e 40				
64 act gct atg	tica gta aaa gaa s	gto oft caa ago tta (Val Leu Gln Ser Leu V ->0					
68 atg gtt gac		gga act tot aat tat t Gly Thr Ser Asn Tyr 1 70	at tog got tit 303				
72 oca adt ada	gor cit cat gca a	agg aaa dat aag tig (Arg Lys His Lys Leu (88					
7m tot dag tig		caa aag cat gea age e Gln Lys His Ala Ser I 190					
80 att gag ada		oga tqt gaa acg gaa q Arg Cys Glu Thr Glu (115					
04 ota gema ama	gad ott tot toa : Glu Leu Ser Ser I	ott ega gae eaa agg ; Leu Arg Asp Glr. Arg (130					
EM gca qua gta	gas asa tad aaa ; Glu Lys Tyr Lys A 145	gad tột gặt dog các ; Asp Cys Asp Pro Gln (150	gtt gig gaa gaa - 543 Val Val Glu Glu				
		god ada gad got got : Ala Lys Glu Ala Ala / 165					
Bri gat auc ata		tot tgg god aaa aga : Ser Trp Ala Lys Arg 180					
100 gaa daa dat ada att gat aga act tit gga att cca gaa gac tit gac 687 101 Glu Glu Asn Eys Ile Asp Arg Thr Phe Gly Ile Pro Glu Asp Phe Asp 102 140 150 200							
104 tac ata rac 1 % Tyr lle As 106	p	gtiggtig langgatigtad nam	gattgtga 736				
	ttitattaat gttaas a		gtogttt geotgtaact 796 aaaaaaa aaaaaaaaaa 956 367				
113 <211 - LENG 114 <012 - TYPE 115 <213 - OR GA 117 <400 - SEQU	: PRT NISM: Homb Sapiens	S					
118 Met Ser Ly. 119 1	s Lys Lys Gly Leu 5	Ser Ala Glu Glu Lys 10 Lys Asp Val Phē Gln	2.5				
1.11	2.)	25 Lys Gly Ile Thr Ala 40	30				

RAW SEQUENCE LISTING 1ATE: SAN 1 *** ATERIT AFFILE ATTENT AFFILE ATTENT US/10/087,190 TIME: In: Elicated at the control of the

light 201 : N:\AMC\087190.txt

Gutput Ser: N:\CRF4\02192003\J087190.raw

124 GD. Val Lou Olfn Ser 125 - 50	Lou Vai	Asp Asp	Gly Met	Val Asp 60	Cys Glu	Arg
126 He Gly Thi Ser Asn 127 65	Tyr Tyr	Crp Ala	Phe Pro 75	Ser Lys	Ala Leu	His 80
128 Ala Arg Lys His Lys 129 8)	Leu Giu	Val Leu	Glu Ser 90	Gln Leu	Ser Glu 95	Gly
120 Ser Gln Lys His Ala 131 100	Ser Leu	Gln Lys 105	Ser l.e	Glu Lys	Ala Lys 110	Ile
102 Gly Arg Cys Glu The 103 115	Glu Glu	Arg Thr	Arg Leu	Ala Lys 125	Glu Leu	Ser
104 Ser Leu Arg Asp Gun 105 130	Arg Glu		Lys A.a	Glu Val 140	Glu Lys	Tyr
106 Lys Asp Cys Asp Pro 107 146	Gln Val 150	Val Glu	G.u I.e 1!5	Arg Gin	Ala Asn	Lys 160
198 Val Ala Lys Glu Ala 199 165	Ala Asr	Arg Trp	The Amp	Asn lle	Phe Ala 175	I 1 @
140 Lyn Ger Trp Ala Lys 140 - 140	Arg Lys	Phe Gly 185	Phe Glu	Glu Asn	Lys lie	A.3p
141 Ard Thr Phe Gly Ile 143 195	Pro Gla	Asp Phe 200	Asp Tyr	Ile Asp 205		
14: -1.10: SEQ ID NO: 4 147-1.11: LENGTH: 1028						
- 148 -0 190 TYPE: DNA - 140 -0 130 ORGANISM: Home	o Sapiens	5				
1: 1 -0.100 FEATURE:						
180 -0.01 NAME/KEY: CDS						
183 - 1.000ATION: (82 187 - 14000 SEQUENCE: 4						66
183 HUMBE LOCATION: (82 187 HANDE SEQUENCE: 4 188 HOMAGAICSA ACCORD	gg gestat	ladag dad				
183 HOUSE LOCATION: (82 187 HANDS SEQUENCE: 4 188 HAMAHATOSA ADJUGUT 187 HAMAHATOSA ADJUGUT	gg gestat gele ata	isaag cad tawaag	айа ана	gga cig	aut gea	gaa 111
183 HUMBE LOCATION: (82 187 HANDE SEQUENCE: 4 188 HOMAGAICSA ACCORD	gg gestat gele ata	ladag dad	айа ана	gga cig	aut gea	gaa 111 Glu 10
183 Higher LOCATION: (82 187 Higher SEQUENCE: 4 189 Devalations adopted 187 grandpoort godocopor 188 189 189	gg godtgt go blatg Met 1 atglatg	loodg ood toa aag Ser Lys gaa ata	add dad Lys Lys ttt tet	gga otg Gly bau gaa aba	aqt gca Ser Ala aaa gat	gaa 111 GLu 10 gta 159
18.8 duffile LOCATION: (82 181 d400) SEQUENCE: 4 18) demandates a adjugated 18 demandaded gardeogod 18 d 18 d 18 d 18 d 18 d 18 d 18 d 18	gg godtgt go blatg Met 1 atglatg	loodg ood toa aag Ser Lys gaa ata	ada ada Lys Lys the ter Phe Ser	gga otg Gly bau gaa aba	aqt gca Ser Ala ada gat Lys Asp	gaa 111 GLu 10 gta 159
183 Himbo LOCATION: (82 187 H4000 SEQUENCE: 4 187 Headatesa acquested 187 Headagescot godecopol 187 187 187 188 161 Had aag aga ast ogo 18. Gin Lys Arg Thr Arg 187	gg gestgt ge e atg Met 1 atg atg Met Met	todog odd tod aag Ser Lys gaa ata Glu Ile	ada ada Lys Lys 50 ttt tet Phe Ser 20	gga otg Gly beu gaa ada Glu Thr	aqt gda Ser Ala aaa gat Lys Asp 28	gaa 111 Glu 10 gta 159 Val
18.8 duffile LOCATION: (82 181 d400) SEQUENCE: 4 18) demandates a adjugated 18 demandaded gardeogod 18 d 18 d 18 d 18 d 18 d 18 d 18 d 18	gg godtgt go o atg Met 1 atg atg Met Met	todog odd tod adg Ser Lys gad ata Glu Ile adg att	add add Lys Lys thi tot Phe Sor 20 get cod	gga otg Gly beu gaa aca Glu Thr	aqt gca Ser Ala ada gat Lys Asp 28 ada ggc	gaa 111 Glu 10 gta 159 Val 207
183 Higher LOCATION: (82 183 Higher SEQUENCE: 4 184 High advantage adjugation 185 Higher and adjugation 185 185 185 186 Higher and adjugate and open 186 Higher and adjugate 186 Pine Glin Deu Lys Asp 186 Higher and App 187 Higher and App	gg gostgt gc c atg Met 1 atg atg Met Met ttg gag Leu Glu	space and ser Lys gaa ata Glu Ile and att Lys Ile 35	ada ada Lys Lys thi tot Phe Ser 20 get ede Ala Pro	gga otg Gly bau gaa ada Glu Thr aaa gag Lys Glu	aqt gca Ser Ala aua gat Lys Asp 25 aua ggo Lys Gly 40	gaa 111 Glu 10 gta 159 Val 207 Ile
183 duffile LOCATION: (82 181 date) SEQUENCE: 4 184 date as adjusted 187 data as a gas 188 data as adjusted 188 da	gg gootgt gc c atg Met l atg atg Met Met ttg gag Leu Glu aaa gaa	specification and ser Lys gas ata Glu Ile asg att Lys Ile 35 gto ott	ada ada Lys Lys thi tot Phe Ser 20 get dec Ala Pro	gga otg Gly bau gaa ada Glu Thr aaa gag Lys Glu tta gtt	aqt gda Ser Ala ada gat Lys Asp 25 ada ggo Lys Gly 40 gat gat	gaa 111 Glu 10 gta 159 Val 207 Ile ggt 255
163 diffine LOCATION: (62 163 diffine EDUENCE: 4 164 diffine SEQUENCE: 4 165 diffined adapted adapted for 165 diffined adapted for 165 diffined adapted for 165 diffined for 165	gg gootgt gc c atg Met l atg atg Met Met ttg gag Leu Glu aaa gaa	toa aag Ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu	ada ada Lys Lys thi tot Phe Ser 20 get dec Ala Pro	gga otg Gly bed gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val	aqt gda Ser Ala ada gat Lys Asp 25 ada ggo Lys Gly 40 gat gat	gaa 111 Glu 10 gta 159 Val 207 Ile ggt 255
183 diffile LOCATION: (82 187 diffile LOCATION: (82 187 diffile SEQUENCE: 4 187 diffile gradient gradeogod 188 199 199 100 diffile and add and ogod 100 diffile Child can the add gao 100 Phe Glin Leu Lys Asp 107 107 diffile got did the gta 170 file Ala Met Ser Val 171 45	gg gestgt ge c atg Met l atg atg Met Met ttg gag Leu Glu aaa gaa Lys Glu	toa aag Ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu 50	ada ada Lys Lys thi tot Phe Ser 20 get coc Ala Pro caa adc Gln Ser	gga otg Gly bed gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val	agt goa Ser Ala aga gat Lys Asp 25 aga ggo Lys Gly 40 gat gat Asp Asp	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly
183 diffine LOCATION: (82 187 diffine EQUENCE: 4 189 diffine SEQUENCE: 4 189 diffine adjustment graphological for graphological graphological for fill gase daig against ogo 10. Girl Lys Arg Thr Arg 10. 15 10% this daid tha ass gad 100 Phe Glin Leu Lys Asp 10% and got atg the gta gta 170 Chr Ala Med Ser Vall 171 45 175 and got gad tigt gag	gg gostgt go c atg Met 1 atg atg Met Met ttg gag Lei Glu aaa gaa Lys Glu agg itd	doog ood toa aag Ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu 50 gga act	ada ada Lys Lys thi tot Phe Sor 20 get coc Ala Pro caa aqo Gln Sor tot aat	gga otg Gly beu gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val 55 tat tat	aqt gda Ser Ala aaa gat Lys Asp 25 aaa ggc Lys Gly 40 gat gat Asp Asp tgg gct	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly 255
183 diffile LOCATION: (82 187 diffile LOCATION: (82 187 diffile SEQUENCE: 4 187 diffile gradient gradeogod 188 199 199 100 diffile and add and ogod 100 diffile Child can the add gao 100 Phe Glin Leu Lys Asp 107 107 diffile got did the gta 170 file Ala Met Ser Val 171 45	gg gostgt go c atg Met 1 atg atg Met Met ttg gag Lei Glu aaa gaa Lys Glu agg itd	doog ood toa aag Ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu 50 gga act	ada ada Lys Lys thi tot Phe Sor 20 get coc Ala Pro caa aqo Gln Sor tot aat	gga otg Gly beu gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val 55 tat tat	aqt gda Ser Ala aaa gat Lys Asp 25 aaa ggc Lys Gly 40 gat gat Asp Asp tgg gct	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly 255 Sly ttt 303 Phe
16.3 diffice LOCATION: (62 16.1 diffice EDUENCE: 4 16.1 diffice SEQUENCE: 4 16.1 difficacioned gogodoogo 16.2 diffice Anglaga ant ogo 16.3 diffice Lys Angl The Anglace The Local tha aka gao 16.4 difficacioned Lys Asplace Anglace The Phe Gle Leu Lys Asplace Anglace The Anglace Anglace The Angla	gg gostgt gc c atg Met l atg atg Met Met ttg gag Lei Glu aaa gaa Lys Glu agg itc Arg Tle 65 cat goa	school coc toa aag Ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu 50 gga act Gly Thr	ada ada Lys Lys tit tot Phe Ser 20 get ede Ala Pro caa age Gln Ser tot adt Ser Aun	gga otg Gly bau gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val 55 tat tat Tyr Fyr 70 ttg gag	aqt gda Ser Ala aaa gat Lys Asp 25 aaa ggc Lys Gly 40 gat gat Asp Asp tgg gct Trp Ala gtt ctg	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly 255 Gly 303 Pne 3351
16.8 differs LOCATION: (62 16.1 d400) SEQUENCE: 4 16.1 demandation and gogodocol 16.1 demandation gogo	gg gootgt gc c atg Met 1 atg atg Met Met ttg gag Leu Glu aaa gas Lys Glu agg atc Arg Cle 65 cat goa His Ala	school coc toa aag Ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu 50 gga act Gly Thr	ada ada Lys Lys tht tot Phe Ser 20 get che Ala Pro caa adc Gln Ser tet adt Ser Ada cat adg His Lys	gga otg Gly bau gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val 55 tat tat Tyr Fyr 70 ttg gag	aqt gda Ser Ala aaa gat Lys Asp 25 aaa ggc Lys Gly 40 gat gat Asp Asp tgg gct Trp Ala gtt ctg	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly 255 Gly 303 Phe 351 Glu 351
16.3 differ LOCATION: (62 16.1 d400 description: 4 16.1 demandation and gogodood 16.1 demandation and gogodood 16.1 demandation and togodood 16.1 demandatio	gg gootgt gc c atg Met 1 atg atg Met Met ttg gag Leu Glu aaa gas Lys Glu agg atd Arg Cle 65 cat gca His Ala 80	space and ser Lys gaa ata Glu Ile aag att Lys Ile 35 gto ott Val Leu 50 gga act Gly Thr agg aaa Arg Lys	ada ada Lys Lys tht tht Phe Ser 20 coo got one Ala Pro caa and Gln Ser tot adt Ser Ada cat adg His Lys 85	gga otg Gly bau gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val b5 tat tat Tyr Fyr 70 ttg gag Leu Glu	aqt gca Ser Ala aaa gat Lys Asp 23 aaa ggo Lys Gly 40 gat gat Asp Asp tgg got Trp Ala gtt ctg Val Leu	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly 255 Gly 303 Phe 351 Glu 90
16.8 differs LOCATION: (62 16.1 d400) SEQUENCE: 4 16.1 demandation and gogodocol 16.1 demandation gogo	gg gootgt gc c atg Met l atg atg Met Met ttg gag Leu Glu aaa gaa Lys Glu agg atd Arg Tle 65 cat goa His Ala 80 tgc tgc	specified and ser Lys gas at a Glu Ile asg att Lys Ile 35 gto ott Val Leu 50 ggs act Gly Thr agg ass Arg Lys tto cat	ada ada Lys Lys tht tht Phe Ser 20 get one Ala Pro caa add Gln Ser tot adt Ser Ada cat adg His Lys 85 gaa ata	gga otg Gly bau gaa ada Glu Thr aaa gag Lys Glu tta gtt Leu Val bb tat tat Tyr Fyr 70 ttg gag Leu Glu att aaa	aqt gda Ser Ala aaa gat Lys Asp 28 aaa ggc Lys Gly 40 gat gat Asp Asp tgg gct Trp Ala gtt ctg Val Leu gtc tcc	gaa 111 Glu 10 gta 159 Val 207 Ile 255 Gly 255 Gly 303 Phe 351 Glu 90 tat 399

RAW SEQUENCE LISTING

HATENT ARRIGNATION: US/10/087,190

lig it itel : N:\AMC\087190.txt

153		41,			100					2		
	tat aga awa the	tigar at a	dera deta	11 G	400	·2a4*	100	tat	aät	ccc	ādd 1	447
_	Tyr Ari Lyr Flor	77.	Tire Ala		*	His	,	Cvs	Ast.	Fit	500	
t	210		,	115				. 1.	120	-		
1.7			_									44
	वटः १६व वृत्व वृत्		gger allake	iasig.	14 J.	qac.		47.4.11	ia Cici	J C 4		4 7 7
190	The Leu Gly Gly											
1 +1	12.5											
11472	cat gaagtigo laada	toggagt to	gtotgagge	j da	jt caa	adag	cate	gcaaq	jaa t	cacac	gaadag	559
	catigagaaa geta											
	gottectica cito											
	ctgtgatccg caag											
	taacagatgg actg											
	tgaaqaaaat aaaa											
1 +9	aaatattoca tggt	ggtgaa go	gatigtiacaa	a got	.tgtq	gaat	atgt	.aaat	. t.t. 1	taaac	tatta	919
21.0	totalictaag tigta	ctgaat to	gtagtitga	cto	gtaac	it.gt	gttt	atca	itt 1	l tatit	.aat.gt	979
	taaataaagt gtaa											1028
	<210: SEQ ID NO											
	<211: LENGTE: 1											
	<2120 TYPE: PRI											
	<213: ORGANISM:	-	oiens									
	<400: SEQUENCE:											
179	Met Ser Lys Lys	Lys Gly	Leu Ser	Ala	Glu	Glu	Lys	Arg	Thr	Arg	Met	
1.10		5			10					15		
	Met Glu Ile Pho	Ser Glu	Thr Lvs	Asp	Val	Phe	Gln	Leu	Lvs	Asp	Leu	
*	20	.551 014	1111 111	25					30	1		
		Dan Inc	Cl., 1.,.		1 7 0	mhx	7 1 a	M ~ +		1751	- ,,,,	
	Glu Lys Ile Ala	PIO Lys		CITÀ	116	111	Ala		JUL	Val	.u.y.s	
1114	3.5		40					45	~	- 1		
11.1.5	G.u Val Leu Glr	. Ser Leu		Asp	Gly	Met		Asp	Cys	31 u	Arg	
	:, 0		55				60					
1117	Tie Gly Thr Ser	Asn Tyr	Tyr Trp	Ala	Phe	Pro	S⊕r	Lys	Ala	Leu	His	
1116	_	70				75					3.0	
	Ala Arg Lys Eis	Lys Leu	Glu Val	Leu	Glu	Ser	Gln	азр	Pro	Glv	Cvs	
1. 0	.ira irag njo na	85			90					95	-	
	Cys Phe His 31c		Time Visl	Sor		Tur	Ara	I • 70	Pho		611	
1	•		rys var		1 9 1	1 7 1	nrg	12 % 12		1 + 1.	اد باد. اد	
41.0	100			105		en. 1		G 1	110			
3	Gly Ala Val Ala	His Ala		Pro	Ser	Thr	Leu		GTA			
11.14	115		120					125				
1. 7	:7 <210: SEQ ID NO: 6											
1.24	114 <211: LENGTH: 1023											
	1.9 <212 · TYPE: DNA											
	230 <213. ORGANISM: Homo Sapiens											
	.320 · FEATURE:											
	<221 · NAME/KEY:											
	<2222 LOCATION:		.(557)									
	<400> SEQUENCE:											
13.	commanteam act	gt mad a	adi at addi	1 12	- it at		maa	raga:	193	zoriji.	garage	60
	ggaagnoot gege											
	actogoatga tigga											
240	aaqattqctc ccaa	ादप्वप्वदित ते	garaf (ac)	gen	.1: (1)	Lay	Cardi	idQde	191		aaaqc	7, 11 17

TIME: 14: "..."

1 20 2

RAW SEQUENCE LISTING

FATENT AFFIL WILLS: US/10/087,190

:::: : N:\AMC\087190.txt

N:\CRF4\02192003\J087190.raw

```
,41 stamtqata arimtarim taa matega paggarogdaa ettemaanta ttamtagget ofk
14% tit svaanta laavit mi ja ilgemägjäämi sätämettiga mettiin jamatetemäämi jed
24 - Est gortgot deficeat la adiaditada instructuit atagadabli etegen ggg : 400
244 adagtiggete ucquetatina teorageart tigggagart garacqqqca gatracqagg 480
24% transittods indicereas at plany typhaag aty gag tig tot gag gga agt 🦙 🤊
                          Met Lys Cys Lys Met Glu Leu Ser Glu Gly Ser
14.
247
                                                                      1, 5, 1
249 caa uug cat, goa ago ota cag aau ugo at! gag auu got uuu att ggo
250 Gin Lys His Ala Ser Leu Gln Lys Ser Ile Glu Lys Ala Lys Ile G.y
                15
                                     20
253 nga tigt gaa ang gaa gag nga abo agg ota goa aaa gag ott tot toa
154 Arg Cys Glu Thr Glu Glu Arg Thr Arg Leu Ala Lys Glu Leu Ser Ser
                                35
                                                                      677
:57 ett eqa gac caa agg gaa cag eta aag gca gaa gta gaa aaa tac aaa
:58 Leu Arg Asp Glr. Arg Glu Gln Leu Lys Ala Glu Val Glu Lys Tyr Lys
                             5()
. 59
        45
                                                                      725
.61 gao tgt gat dog dua git gig gaa gaa ata dgo daa goa aat aaa gita
162 Asp Cys Asp Pro Gln Val Val Glu Glu Ile Arj Gln Ala Asn Lys Val
..63 60
                         65
                                             7:)
.65 gec aaa gaa get get aac aga tgg aet gat aac ata tte gea ata aaa
.66 Ala Lys Glu Ala Ala Asn Arg Trp Thr Asp Asn Ile Phe Ala Ile Lys
                    8.0
                                        5 ع
169 tot tgg god aaa aga aaa tit ggg tit gaa gaa aat aaa ait gat aga
                                                                      821
.70 Ser Trp Ala Lys Arg Lys Phe Gly Phe Glu Glu Asn Lys Ile Asp Arg
                95
                                    100
                                                                      867
.73 act tit gga att oca gaa gad tit gad tad ata gad taaaatattd
.74 Thr Phe Gly Ile Pro Glu Asp Phe Asp Tyr Ile Asp
                                115
          110
.77 datggtggtg aaggatgtad aagdttgtga atatgtaaat titaaadtat tatdtaadta 927
78 agtglactga attgtcgttt gootgtaact gtgtttatca ttttattaat gttaaaataaa 987
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.82 <211> LENGTH: 119
.:83 <212> TYPE: PRT
.:84 <213 > ORGANISM: Homo Sapiens
.:86 <:400> SEQUENCE: 7
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289 Leu Gln Lys Ser Ile Glu Lys Ala lys Ile Gly Arg Cys Glu Thr Glu
                                    25
               20
291 Gla Arg Thr Arg Lea Ala Lys Glu Leu Ser Ser Leu Arg Asp Glr Arg
            35
                                40
293 Glu Gin Leu Lys Afa Glu Val Glu Lys Tyr Lys Asp Cys Asp Fro Gln
                            55
294 50
195 Val Val Glu Glu Ilo Ard Uln Ala Ash Lys Val Ala Lys Glu Ala Ala
                                            75
297 Asn Arg Trp Thr Asp Asn Ile Fhe Ala Ile Lys Ser Trp Ala Lys Arg
                                        90
2 of Lys The Gly The Glo Glo Glo Aen Lys Ile Aen And Tho Phe Ely Ile Fro
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RAW SEQUENCE LISTING ERROR SUMMARY

Thirt: ", IN", -TIMB: 19:80:20

FATENT APPLY WATER N: US/10/087,190

ligat Set : N:\AMC\087190.txt Output Set: N:\CRF4\02192003\J087190.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:29; Xaa Fos. 1,3,13